



PCT09

## RAW SEQUENCE LISTING

DATE: 01/24/2002

PATENT APPLICATION: US/09/890,752A

TIME: 13:37:59

Input Set : A:\107070-120.ST25.txt

Output Set: N:\CRF3\01242002\I890752A.raw

PS  
ENTERED

4 <110> APPLICANT: Hildt, Eberhard  
 5 Hofschneider, Peter  
 7 <120> TITLE OF INVENTION: Particles for Gene Therapy  
 9 <130> FILE REFERENCE: 107070-120 (VOS-013)  
 11 <140> CURRENT APPLICATION NUMBER: US 09/890,752A  
 12 <141> CURRENT FILING DATE: 2001-08-03  
 14 <150> PRIOR APPLICATION NUMBER: PCT/DE00/00363  
 15 <151> PRIOR FILING DATE: 2000-02-04  
 17 <150> PRIOR APPLICATION NUMBER: DE 199 04 800.2  
 18 <151> PRIOR FILING DATE: 1999-02-05  
 20 <160> NUMBER OF SEQ ID NOS: 21  
 22 <170> SOFTWARE: PatentIn version 3.1  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 347  
 26 <212> TYPE: PRT  
 27 <213> ORGANISM: Artificial Sequence  
 29 <220> FEATURE:  
 30 <223> OTHER INFORMATION: Fusion protein comprising a LHBS and heterologous binding  
 31 site RGD  
 33 <400> SEQUENCE: 1  
 35 Met Gly Arg Gly Asp Gly Ala Gly Ala Phe Gly Leu Gly Phe Thr Pro  
 36 1 5 10 15  
 38 Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln Ala Gln Gly Ile Leu  
 39 20 25 30  
 41 Glu Thr Leu Pro Ala Asn Pro Pro Pro Ala Ser Thr Asn Arg Gln Ser  
 42 35 40 45  
 44 Gly Arg Gln Pro Thr Pro Leu Ser Pro Pro Leu Arg Asn Thr His Pro  
 45 50 55 60  
 47 Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His Gln Thr Leu Gln Asp  
 48 65 70 75 80  
 50 Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly  
 51 85 90 95  
 53 Thr Val Asn Pro Val Pro Thr Thr Val Ser Pro Ile Ser Ser Ile Phe  
 54 100 105 110  
 56 Ser Arg Ile Gly Asp Pro Ala Leu Asn Met Glu Asn Ile Thr Ser Gly  
 57 115 120 125  
 59 Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr  
 60 130 135 140  
 62 Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu  
 63 145 150 155 160  
 65 Asn Phe Leu Gly Gly Thr Thr Val Cys Leu Gly Gln Asn Ser Gln Ser  
 66 165 170 175  
 68 Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Thr Cys Pro Gly

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69          180          185          190
71 Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu
72          195          200          205
74 Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met
75          210          215          220
77 Leu Pro Val Cys Pro Leu Ile Pro Gly Ser Ser Thr Thr Ser Thr Gly
78 225          230          235          240
80 Pro Cys Arg Thr Cys Thr Thr Pro Ala Gln Gly Thr Ser Met Tyr Pro
81          245          250          255
83 Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro
84          260          265          270
86 Ile Pro Ser Ser Trp Ala Phe Gly Lys Phe Leu Trp Glu Trp Ala Ser
87          275          280          285
89 Ala Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe
90          290          295          300
92 Val Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp
93 305          310          315          320
95 Tyr Trp Gly Pro Ser Leu Tyr Ser Ile Leu Ser Pro Phe Leu Pro Leu
96          325          330          335
98 Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
99          340          345
103 <210> SEQ ID NO: 2
104 <211> LENGTH: 215
105 <212> TYPE: PRT
106 <213> ORGANISM: Artificial Sequence
108 <220> FEATURE:
109 <223> OTHER INFORMATION: Fusion protein comprising a HBcAg, a cell-permeability-
110      mediating polypeptide and heterologous binding site RGD
113 <400> SEQUENCE: 2
115 Met Pro Leu Ser Ser Ile Phe Ser Arg Ile Gly Asp Pro Thr Val Gln
116 1          5          10          15
118 Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile Asp Pro
119          20          25          30
121 Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu Pro Ser
122          35          40          45
124 Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser Ala Leu
125          50          55          60
127 Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His His Thr
128 65          70          75          80
130 Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr Leu Ala
131          85          90          95
133 Thr Trp Val Gly Val Asn Leu Glu Asp Pro Glu Phe Arg Gly Asp Ala
134          100          105          110
136 Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
137          115          120          125
139 Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
140          130          135          140
142 Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
143 145          150          155          160

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145 Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
146                               165                               170                               175
148 Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
149                               180                               185                               190
151 Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser
152                               195                               200                               205
154 Gln Ser Arg Glu Pro Gln Cys
155                               210                               215
160 <210> SEQ ID NO: 3
161 <211> LENGTH: 663
162 <212> TYPE: DNA
163 <213> ORGANISM: Artificial Sequence
165 <220> FEATURE:
166 <223> OTHER INFORMATION: DNA coding for a fusion protein comprising a HBCAg, a
167 cell-permeability-mediating polypeptide and heterologous
168 binding site RGD
170 <400> SEQUENCE: 3
171 atgcccatat cgtaaatctt ctcgaggatt ggggaccctg gatccactac tgttcaagcc      60
173 tccaagctgt gccttggggtg gctttggggc atggacatcg acccttataa agaatttgga      120
175 gctactgtgg agttactctc gtttttgccct tctgacttct ttccttcagt acgagatctt      180
177 ctagataaccg cctcagctct gtatcgggaa gccttagagt ctctgagca ttgttcacct      240
179 caccatactg cactcaggca agcaattctt tgctgggggg aactaatgac tctagctacc      300
181 tgggtgggtg ttaatttgga agatccagaa ttccgaggcg acgcgtctag agacctagta      360
183 gtcagttatg tcaacactaa tatgggccta aagtccaggc aactcttggt gtttcacatt      420
185 tcttgctctc cttttggaag agaaaccggt atagagtatt tgggtgtctt cggagtgtgg      480
187 attcgcactc ctccagctta tagaccacca aatgccccta tcctatcaac acttccggaa      540
189 actactgttg ttagacgacg aggcaggtcc cctagaagaa gaactccctc gcctcgaga      600
191 cgaaggtctc aatcgccgcg tcgcagaaga tctcaatctc gggaacctca atgttagtat      660
193 tcc                                                                                   663
197 <210> SEQ ID NO: 4
198 <211> LENGTH: 1047
199 <212> TYPE: DNA
200 <213> ORGANISM: Artificial Sequence
202 <220> FEATURE:
203 <223> OTHER INFORMATION: DNA coding for a fusion protein comprising a LHBS and
204 heterologous binding site RGD
206 <400> SEQUENCE: 4
207 atgggcccgtg gcgaaggagc tggagcatte gggctggggt tcaccccacc gcacggaggc      60
209 cttttgggggt ggagccctca ggctcagggc atactacaaa ctttgccagc aaatccgcct      120
211 cctgcctcca ccaatcgcca gacaggaagg cagcctaccc cgtgtctcc acctttgaga      180
213 aacactcatc ctcaggccat gcagtggaat tccacaacct ttcaccaaac tctgcaagat      240
215 ccagagtga gaggcctgta tttccctgct ggtggctcca gttcaggagc agtaaaccct      300
217 gtcccgacta ctgctctctc cttatcgta atcttctcga ggattgggga ccttcgctg      360
219 aacatggaga acatcacatc aggattccta ggacccttc tcgtgttaca ggcggggttt      420
221 ttcttggtga caagaatcct cacaataccg cagagtctag actcgtggtg gacttctctc      480
223 aattttctag ggggaactac cgtgtgtott ggccaaaatt cgcagtcccc aacctccaat      540
225 cactcaccaa cctctgttcc tccaacttgt cctggttate gctggatgtg tctgcggcgt      600
227 tttatcatct tcctcttcat cctgctgcta tgctcatct tcttggtggt tcttctggac      660
229 tatcaaggta tgttgcccggt ttgtcctcta attccaggat cctcaaccac cagcacggga      720

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231 ccatgccgaa cctgcatgac tactgctcaa ggaacctcta tgtatccctc ctgttgctgt      780
233 accaaacctt cggacggaaa ttgcacctgt attcccatcc catcatcctg ggctttcgga      840
235 aaattcctat gggagtgggc ctcagcccggt ttctcctggc tcagtttact agtgccattt      900
237 gttcagtggt tcgtaggggt ttcccccaact gtttggtttt cagttatatg gatgatgtgg      960
239 tattgggggc caagtctgta cagcatcttg agtccctttt taccgctgtt accaattttc     1020
241 ttttgtcttt gggatatacat ttaaacc                                     1047
244 <210> SEQ ID NO: 5
245 <211> LENGTH: 35
246 <212> TYPE: DNA
247 <213> ORGANISM: Artificial Sequence
249 <220> FEATURE:
250 <223> OTHER INFORMATION: Primer
252 <400> SEQUENCE: 5
253 ccatattctt gggaacaaga tatccagcac ggggc                                35
256 <210> SEQ ID NO: 6
257 <211> LENGTH: 33
258 <212> TYPE: DNA
259 <213> ORGANISM: Artificial Sequence
261 <220> FEATURE:
262 <223> OTHER INFORMATION: Primer
264 <400> SEQUENCE: 6
265 ggattgctgg tggaagatat ctgccccgtg ctg                                33
269 <210> SEQ ID NO: 7
270 <211> LENGTH: 33
271 <212> TYPE: DNA
272 <213> ORGANISM: Artificial Sequence
274 <220> FEATURE:
275 <223> OTHER INFORMATION: Primer
277 <400> SEQUENCE: 7
278 cagcacgggg cagatatctt ccaccagcaa tcc                                33
281 <210> SEQ ID NO: 8
282 <211> LENGTH: 38
283 <212> TYPE: DNA
284 <213> ORGANISM: Artificial Sequence
286 <220> FEATURE:
287 <223> OTHER INFORMATION: Primer
289 <400> SEQUENCE: 8
290 gccccgtgct ggatatcatc ttgttcccaa gaatatgg                            38
293 <210> SEQ ID NO: 9
294 <211> LENGTH: 36
295 <212> TYPE: DNA
296 <213> ORGANISM: Artificial Sequence
298 <220> FEATURE:
299 <223> OTHER INFORMATION: Primer
301 <400> SEQUENCE: 9
302 aaaagatctg gccgtggcga aggagctgga gcattc                            36
305 <210> SEQ ID NO: 10
306 <211> LENGTH: 30
307 <212> TYPE: DNA

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308 <213> ORGANISM: Artificial Sequence
310 <220> FEATURE:
311 <223> OTHER INFORMATION: Primer
313 <400> SEQUENCE: 10
314 aaaagatctg gtttaaagt atacccaaag 30
317 <210> SEQ ID NO: 11
318 <211> LENGTH: 33
319 <212> TYPE: DNA
320 <213> ORGANISM: Artificial Sequence
322 <220> FEATURE:
323 <223> OTHER INFORMATION: Primer
325 <400> SEQUENCE: 11
326 cccgatatca tgcacatctt tggatcatgta cta 33
329 <210> SEQ ID NO: 12
330 <211> LENGTH: 30
331 <212> TYPE: DNA
332 <213> ORGANISM: Artificial Sequence
334 <220> FEATURE:
335 <223> OTHER INFORMATION: Primer
337 <400> SEQUENCE: 12
338 ggggatatcg gtcgatgtcc atgccccaaa 30
341 <210> SEQ ID NO: 13
342 <211> LENGTH: 36
343 <212> TYPE: DNA
344 <213> ORGANISM: Artificial Sequence
346 <220> FEATURE:
347 <223> OTHER INFORMATION: Primer
349 <400> SEQUENCE: 13
350 ggggatatccc gatgtacggg ccagatatat gcggtt 36
353 <210> SEQ ID NO: 14
354 <211> LENGTH: 27
355 <212> TYPE: DNA
356 <213> ORGANISM: Artificial Sequence
359 <220> FEATURE:
360 <223> OTHER INFORMATION: Primer
362 <400> SEQUENCE: 14
363 ggggatatccg cggcgcgttt acttgta 27
366 <210> SEQ ID NO: 15
367 <211> LENGTH: 57
368 <212> TYPE: DNA
369 <213> ORGANISM: Artificial Sequence
371 <220> FEATURE:
372 <223> OTHER INFORMATION: Primer
374 <220> FEATURE:
375 <221> NAME/KEY: misc_feature
376 <222> LOCATION: (1)..(57)
377 <223> OTHER INFORMATION: Nucleotides 1-3 and 55-57 are "n" wherein "n" = any
nucleotide.
379 <400> SEQUENCE: 15
380 nnnagatcta tgcccatatc gtcaatcttc tcgaggattg gggaccctgg atccnnn 57

```

Use of n and/or Xaa has been detected in the Sequence Listing.  
 Review the Sequence Listing to insure a corresponding  
 explanation is presented in the <220> to <223> fields of  
 each sequence using n or Xaa.

## VERIFICATION SUMMARY

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Input Set : A:\107070-120.ST25.txt

Output Set: N:\CRF3\01242002\I890752A.raw

L:380 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
L:397 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
L:414 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:431 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:449 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19